

FIG. 1

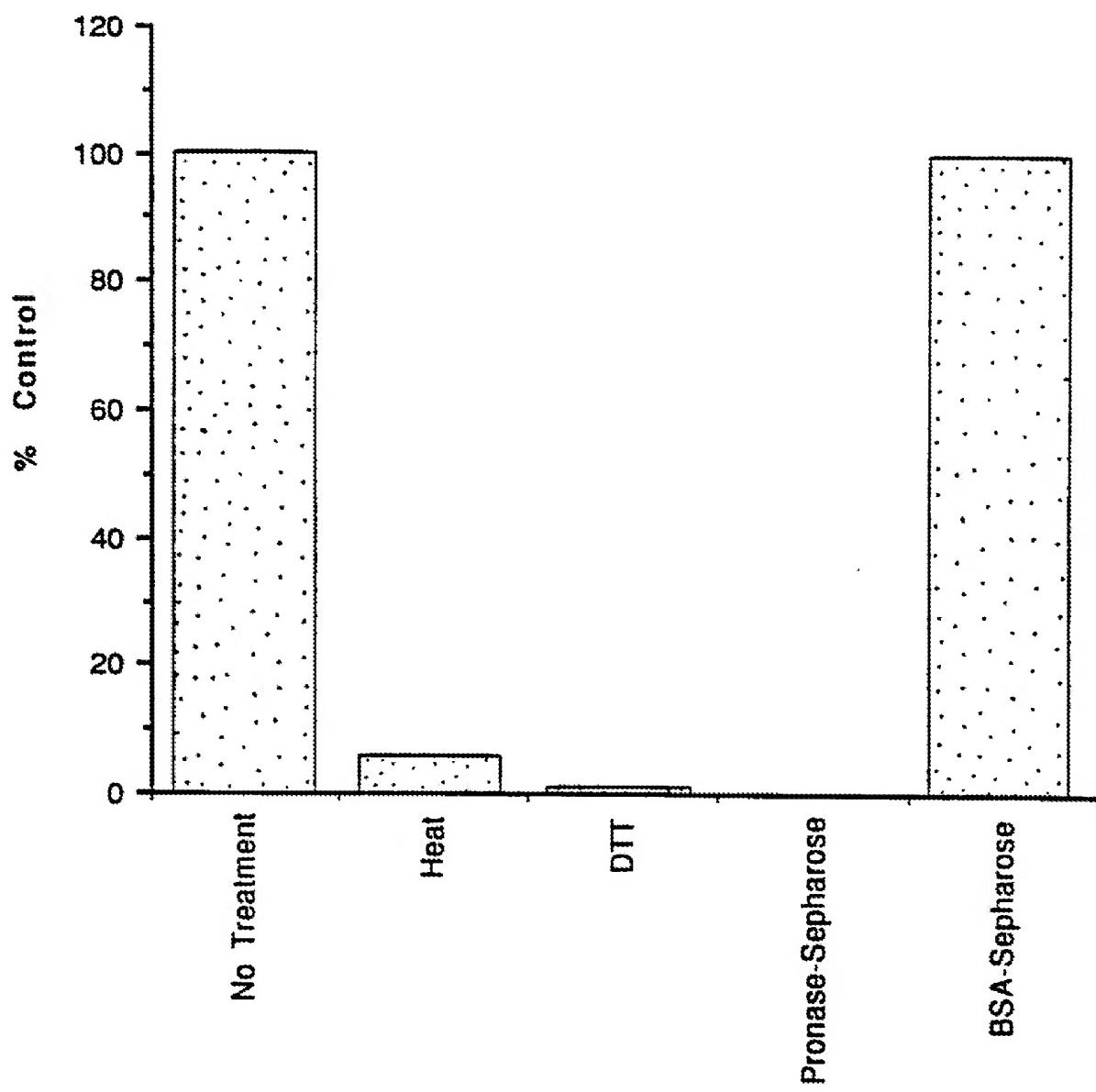


FIG. 2

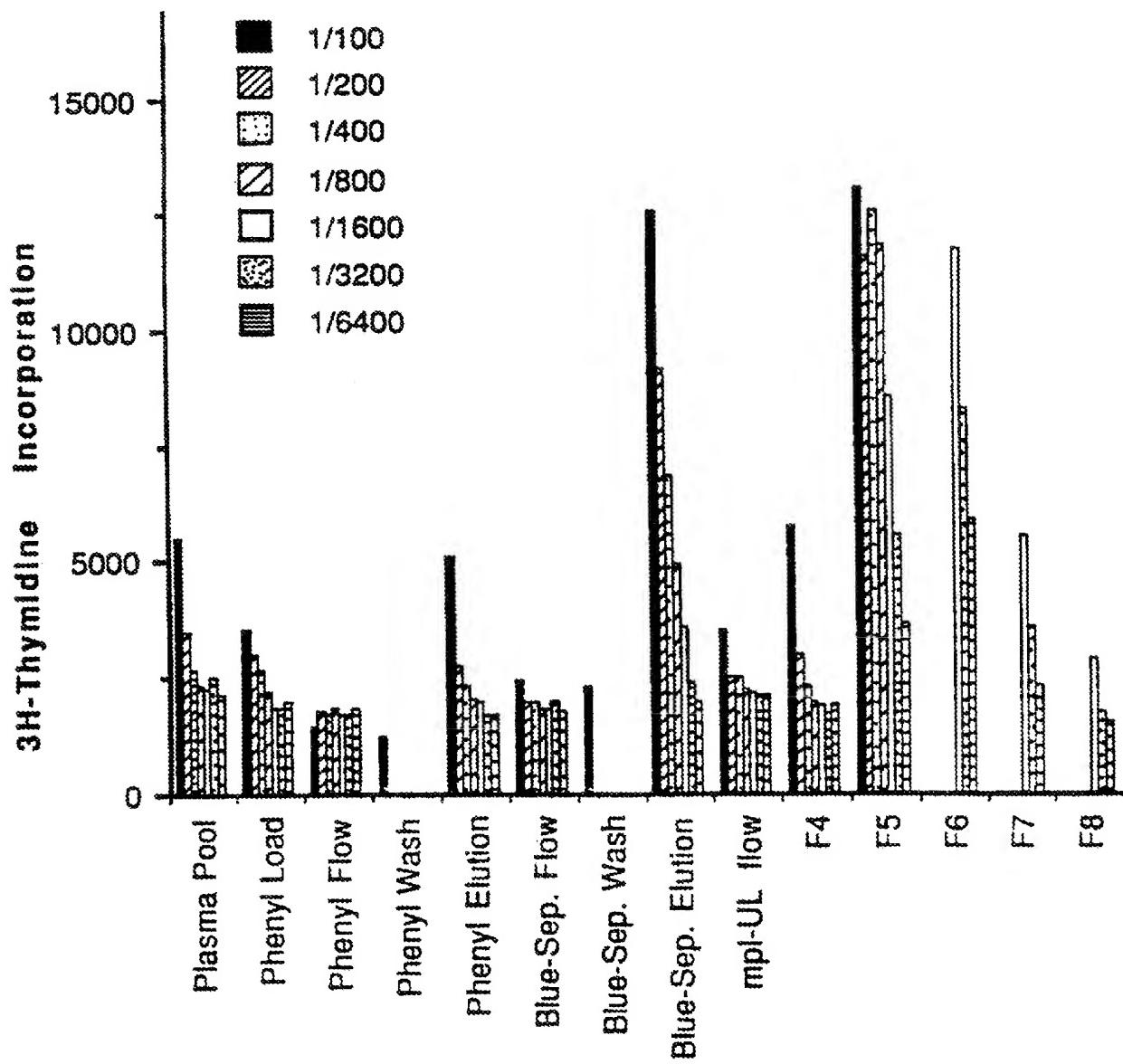


FIG. 3

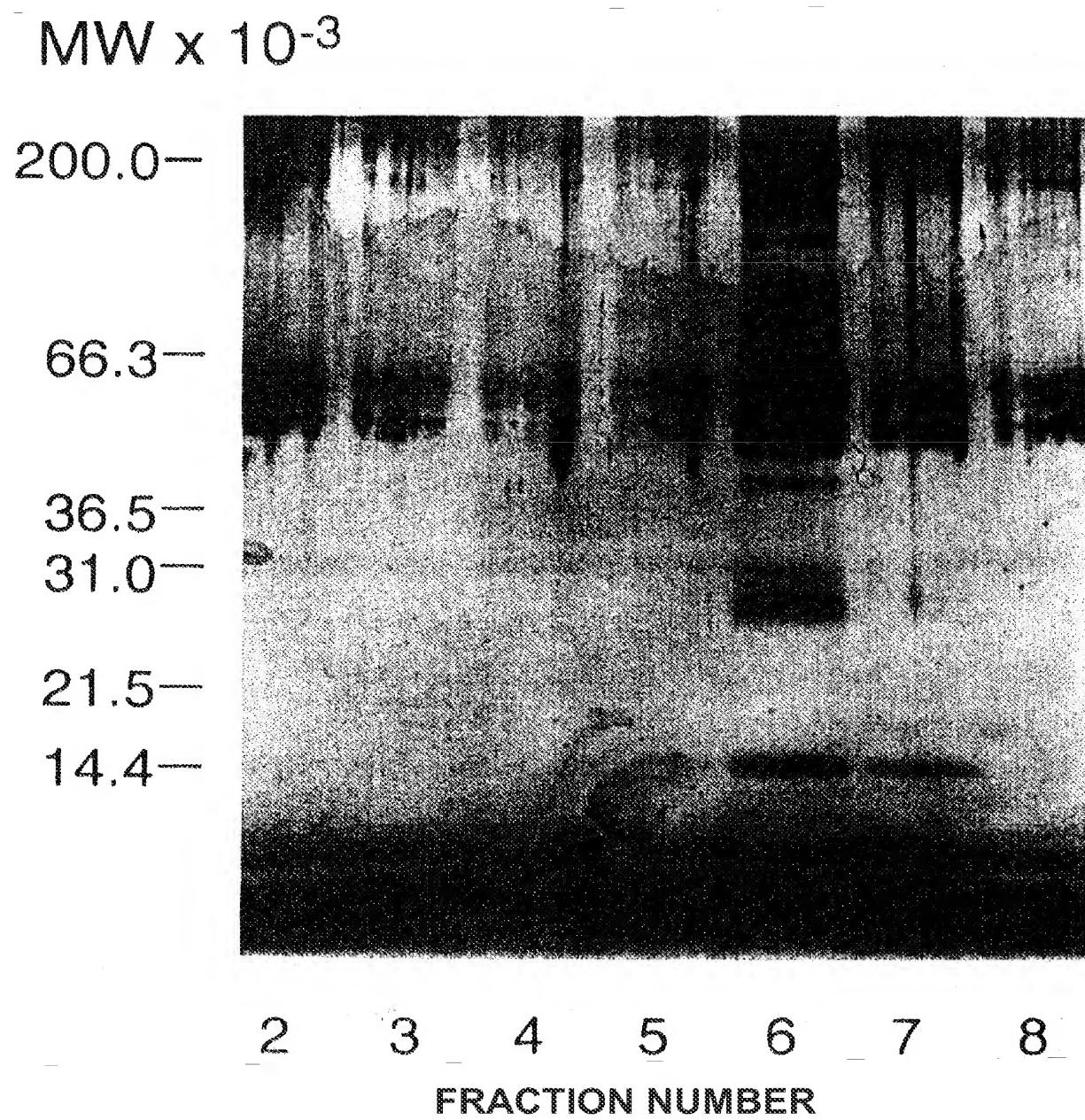


FIG. 4

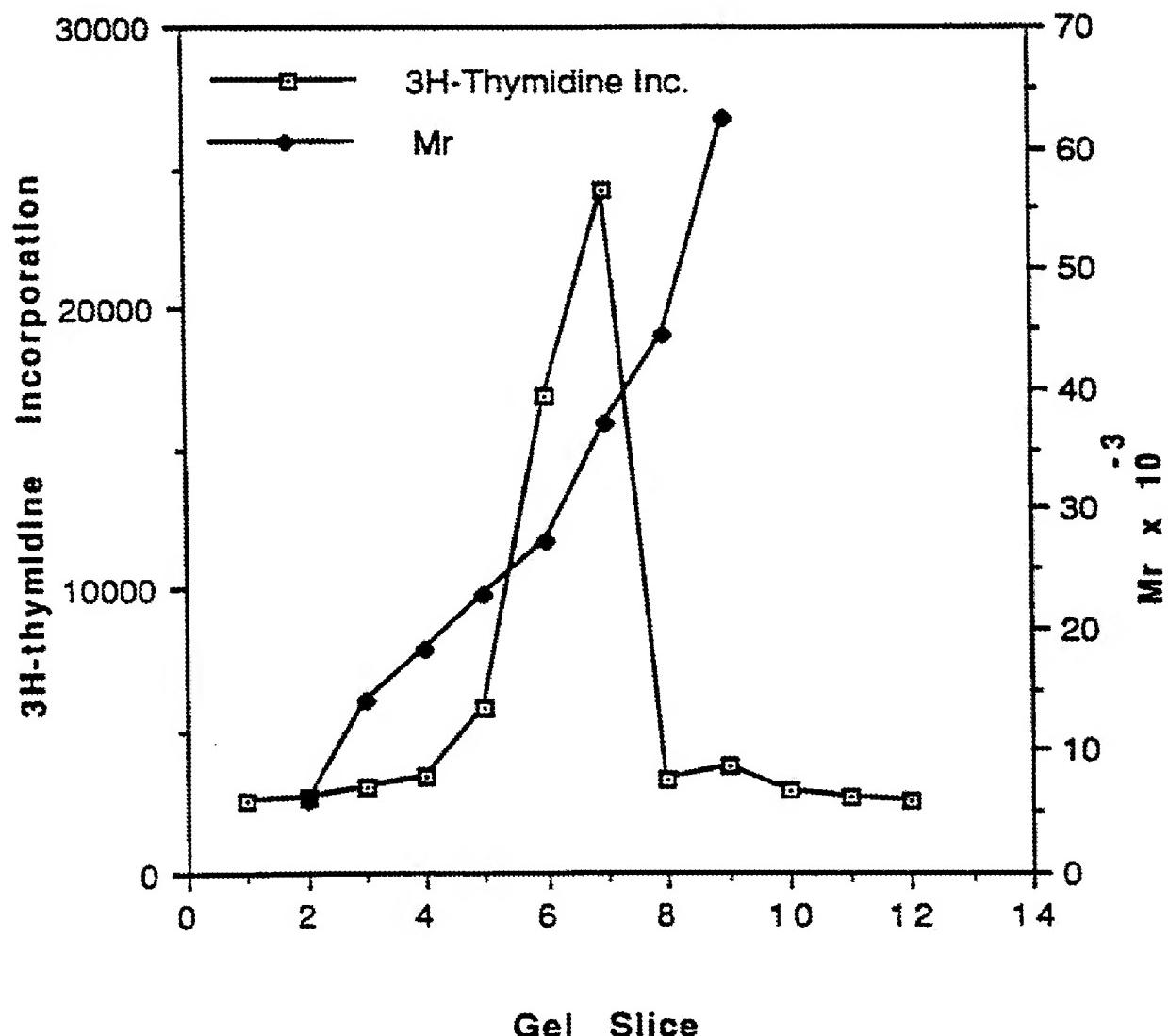


FIG. 5

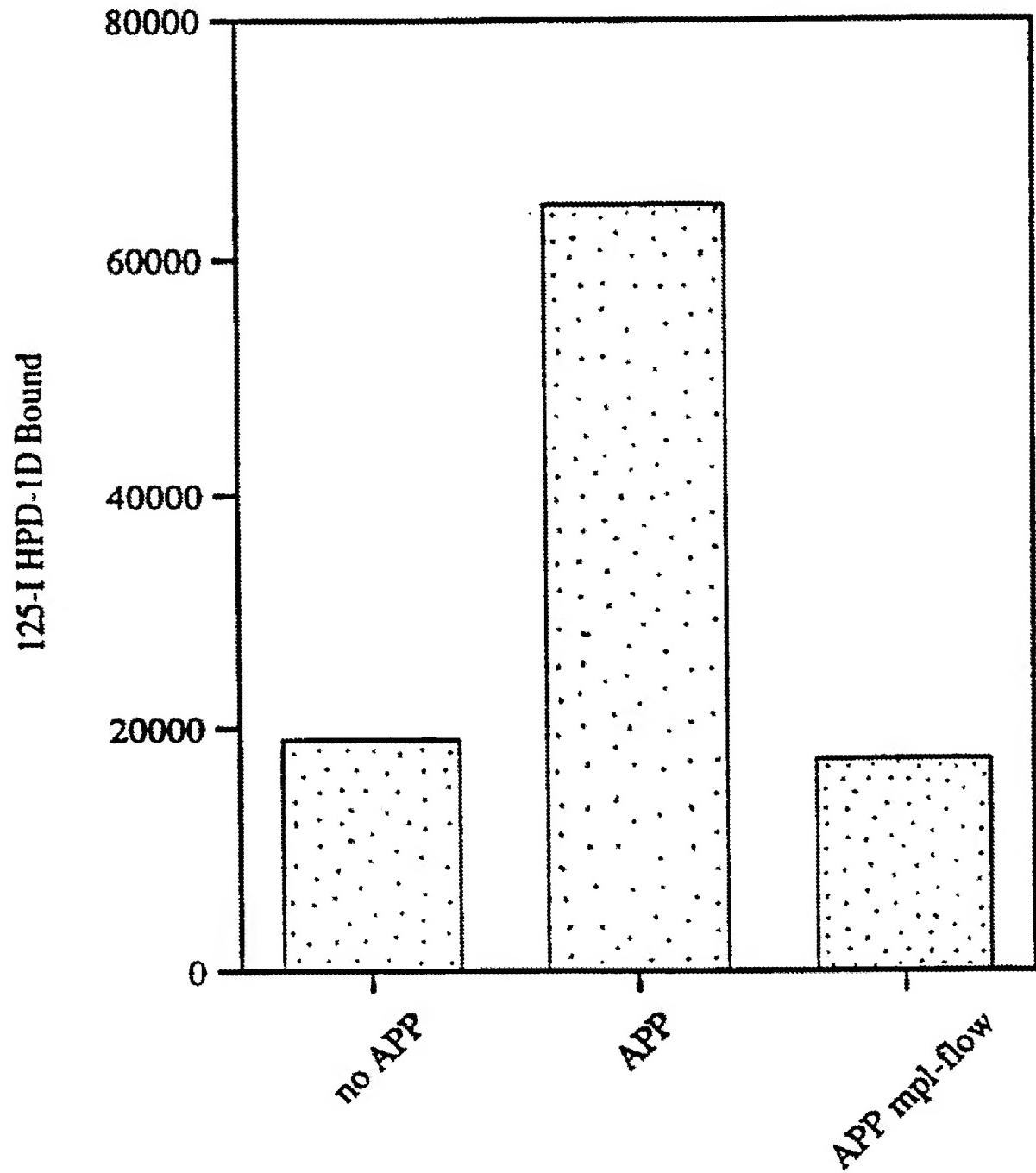


FIG. 6

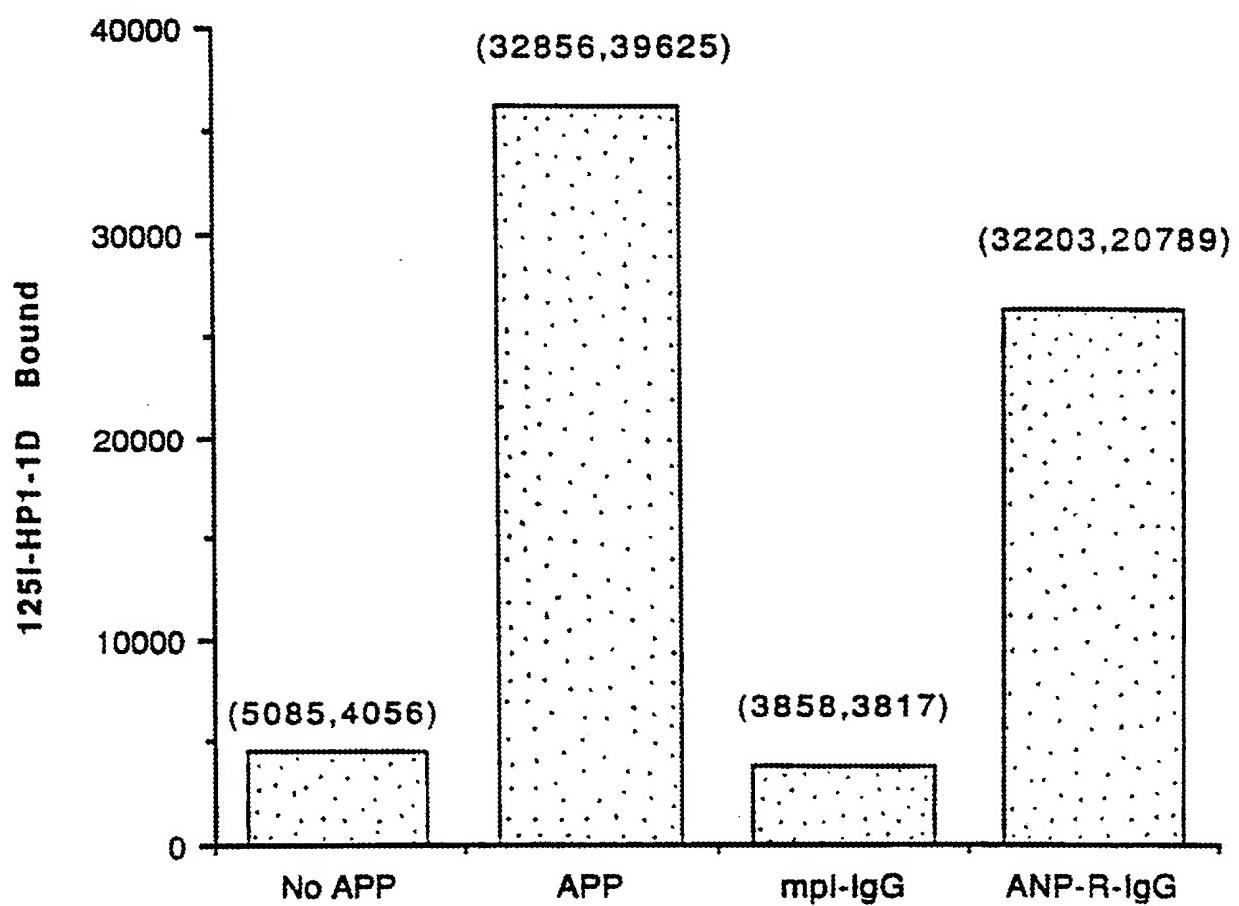


FIG. 7

1 GAATTCCCTGG AATACCGCT GACAATGATT TCCTCCCTCAT CTTTCAACCT CACCTCTCCT CATCTAAGAA -10
CTTAAGGACC TTATGGTCGA CTGTTACTAA AGGGGAGTA GAAAGTTGGA GTGGAGAGGA GTAGATCTT AACGAGGAGC ACCAGTACGA AGAGGATTGA

10 A R L T L S S P A P A C D L R V L S K L L R D S H V L H S R L
101 GCAAGGCTAA CGCTGTCCAG CCCGGCTCCT CCTGCTTGTG ACCTCCGAGT CCTCAGTAAA CTGCTTGTG ACTCCCATGT CCTTCACAGC AGACTGGTA
CGTTCCGATT GGCACAGGTG GGACGAACAC TGAGGGCTCA GGAGGTACG TGAGGGTACA GGAAAGGTCA TGTTGACCT

20 10 GACACCCATA CTCCCAGGAA GACACCATCA CTTCCTCTAA CCTCCTGACC CAATGACTAT
201 GAACTCCCAA CATTATCCCC TTTATCCGG TAACCTGGTAA GACACCCATA CTCCCAGGAA GACACCATCA CTTCCTCTAA CCTCCTGACC CAATGACTAT
CTTGAGGGTT GTAATAGGG AAATAGGGC ATTGACCATT CTGTGGTAT GAGGGTCTT CTGTGGTAGT GAAGGAGAT GAGGAAGTGG GTTACTGATA

301 TCTTCCATA TTGTCCCAC CTACTGATCA CACTCTGTA CAAGAATTAT TCTCACAAT ACAGGCCGCA TTAAAAGCT CTCGCTAGA
AGAAGGGTAT AACAGGGGTG GATGACTAGT GTGAGAGCT GTTCTTATA AGAAGTGTAA TGTGGGGGTAA AAATTTCGA GAGCAGATCT

1	GGGCTTCCT ACCCATCTGC TCCCCAGAGG GCTGCCGCT GTGCACCTGG CCCCCTCCAC CCCGATAGAT TCCCTCACCC TGGCCGGCT	GGAGAGGTG CAGGACTCG CACGTGAACC CAGGAGGA ACCGGGGAA
101	TTGGCCACC CTACTCTGCC CAGAACTGCA AGAGCCCTAAC CGGCCCTCAT GCCCCAGGA AGGATTCAAGG CCTCTAACGTC	GGGGAGGTA CGGGGGCTT AGGAGTGGGA AGGAGTCTA ACCGGGGAA
	-20 Me tGluLeuThr GluLeuLeuL euValValMe tLeuLeuLeu ThrAlaArgL euThrLeuSe rSerProAla ProProAlaCys	1
201	CCAGACACCC CGGCCAGAAAT GGAGCTGACT GAATTGCTCC TGGTGGTCA AGAACAGTA	TCGTTGGTCAT GCTTCTCTTA ACCTGAAAGGC TAACGTTGGC
	10	10
301	AspLeuAla qValLeuSer LysLeuLeuA rqAspSerHi sValLeuHis SerArgLeuS ergInCysPr ogluVa1His ProLeuProT hrProValLeu	TGTCCCTCAC AGCAGACTGA GCCAGTCCCC AGAGGTTCAC CACCTGCTCTA
	20	20
401	LeuProAla ValAspPheS erLeuGlyGlnTrpLysThr GluMetGluGluTrpLysSerAlaThrLysAlaValAspIle LeuGlyAlaV	GCTGGCTGGT GTCGACTTTA GCTGGGAGA ATGGAAAACC CAGATGGGG AGACCAAAGG AGCAGACTGA TGTCTGACT
	50	50
501	ValMetAlaA IaArgGlyGlnTrpLysPro ThrCysLeuS erSerLeuL uGlyGlnLeu SerGlyGlnV aArgLeuL uleuGlyAla LeuGlySerLeu	GTCGATGGCAG CACGGGACA ACTGGGACCC ACTTGGCTCT CATCCCTCCT GGGGAGGCTT TCTGGACAGG
	80	90
601	LeuGlyTh rGlnLeuPro ProGlnGlyA rgThrThrAl aHisLysAsp ProAsnAlaI lepheLeuSe rPheGlnHis LeuLeuArgG lyLysValArg	TGGCTGGAAC CCAGCTTGGCT CCACAGGGCA GGACCAAGGC TCACAAGGAT CCCAATGGCA AGTGGTCTCA GGGTTACGGT AGAAGGACTC
	110	120
701	PheLeuMet LeuValGlyGlySerThrLeucysValArg ArgAlaProP roThrThrAl aValProSer ArgThrSerL euValLeuIhrLeuAsnGlu	TTTCCCTGATG CTGTAGGAG GGTCAACCT CTGGCTCAGG GGGCCCCAC CCACCAAGC TGTCCTCAC TAGTCCTCAC
	140	130
801	LeuProAsnA rgThrSerAl yLeuLeuGlu Thrasnhet hraAlaSerAl aArgThrThr GlySerGlyL euLeuLystr pGlnGlnGly PheArgAlaLys	CTCCCAAAACA GGACTCTGG ATTGTGGAG ACAAAACTCA CCTGAAGACC TAACAAACCTC TGTGTGAACT
	180	190

Figure 8a

210 IleProGlyLeuAsn GluThrSerA rgSerLeuAsn pgInIlePro GlyTyrLeuA snArgIleHi sGluLeuLeu AsnGlyThra rgGlyLeuPhe
901 AGATTCCTGG TCTGCTGAAC CAAACCTCCA GGTCCCTGGGA CCAATCCCC GGATACCTGA ACAGGATACA CGAACCTTG ATGGAACCTC GTGGACTCTT
TCTAAGGACC AGACGACTTG GTTTGGAGGT CCAGGGACCT GTTTAGGG CCTATGGACT TGTCTATGT TTACCTTGAG CACCTGAGAA 240

220 ProGlyPro SerArgArgT hrLeuGlyAl aProAspIle SerSerGlyT hrSerAspTh rglySerLeu ProProAsnL euGlnProGly yTyrSerPro
1001 TCTGGACCC TCACCGAGGA CCTTAGGAGC CCCGACATT TCTCAGGAA CATCAGACAC AGGCTCCCTG CCACCAAACC TCCAGCCTGG ATATTCTCCT
AGGACCTGGG AGTGCCTGCC AGGATCCTCG GGGCTGTAA AGGAGTCCTT GTAGTCTGTG TCCGAGGGAC GGTGGTTGG AGGTGGACCC TATAAGGAGA 260

230 SerProThrH isProProTh rglyGlnTyr ThrLeuPheP roLeuProPr oThrLeuPro ThrProValV alGlnLeuHi sProLeuLeu ProAspProSer
1101 TCCCCAACCC ATCCCTCTAC TGACAGTAT ACGCTCTTCC CTCCTCCACC CACCTGCC ACCCTGTGG TCCAGCTCCA CCCCTGTT CCTGACCCCT
AGGGTTGGG TAGGAGGATG ACCTGTCTATA TGCAGAACGGG GTGGAAACGGG TGGGAAGGTGG GAGAAGGAGG AGGTGAGGT GGACTGGGAA 280

240 AlaProTh rProThrPro ThrSerProL euLeuAsnTh rSerTyrThr HisSerGlnA snLeuSerGly nGluGly
1201 CTGCTCCAAC GCCCACCCCT ACCAGCCCTC TTCTAAACAC ATCCTACACC CACTGCCAGA ATCTGTCAGA GGAAGGGTAA GTTCTCAGA CACTGCCAG
GACGAGGTTG CGGGTGGGA TGGTGGGA AAGATTTGTG TAGGATGTG GTGAGGGTCT TAGACAGAGT CCTTOCCATT CCAAGAGTCT GTGAGGGCTG
1301 ATCAGCATTG TCTCATGTAC AGCTCCCTC CCTGCAAGGGC GCCCCTGGGA GACAACCTGGA CAAGATTTCC TACTTCTCC TGAACACCAA AGCCCCTGGTA
TAGTCGTAAC AGAGTACATG TGGAGGGAA GGACGCCCTGGGGACCC CTGTGACCT GTTCTAAAGG ATGAAAGAGG ACTTTGGTT TCGGGACCAT 300

250 Al aProTh rProThrPro ThrSerProL euLeuAsnTh rSerTyrThr HisSerGlnA snLeuSerGly nGluGly
1401 TTTCCCTATG TGTCCCTGACT TTTCCCTAG TAAAAGTGA CATGTAATAT TTGGAGTCT ACATGCTCTT TTTCTGTGAT AACTGTCAA AGGCTGGC TGGCTGGCA
CTAGCTCTT GGTCTATTTT CTGCAACTCA TTGCAAAAT AACGTTGAGT GACTAAGAGA TGTAGAGAA AAAGACACTA TTGAGACGTT TCCGGACCCG ACCGGACCGT
GATCGAGAAA CCAGATAAAAG GAGGTCTTT AACGTTGAGT GACTAAGAGA TGTAGAGAA AAAGACACTA TTGAGACGTT TCCGGACCCG ACCGGACCGT 320

260 GTTGAACAGA GGGAGAGACT AACCTTGAGT CAGAAAACAG AGAAAAGGTAA ATTTCCTTGG CTTCAAATTTC AAGGCCTTCC AACGCCCTTCA TCCCCTTAC
CAACCTGTCT CCCTCTGTGA TTGGAACTCA GTCTTTGTC TCTTCCAT TAAAGAAAC GAAGTTTAAAG TCCGGAGGGT AGGGAAATG 340

270 GTTGAACAGA GGGAGAGACT AACCTTGAGT CAGAAAACAG AGAAAAGGTAA ATTTCCTTGG CTTCAAATTTC AAGGCCTTCC AACGCCCTTCA TCCCCTTAC
ATAGTAAGAG TCACCTGTGAG ACTAGGGTAT AAGAATGTGAG AACTCTTAC TTATTGCAA GAGAGCTTTT TTTTTTTTTT TTTTTTTT 360

Figure 8b

hmp11	1	· · · · ·	M E L T E [L][L] V V M L [L] T A R L T [L] S S P APP A [C D] L [R V L] S K L [L] R D S H V L H
hepo	1	M G V H E C P A W L W [L][L]	S L L S [L] P L G L P V [L] G A P P R L I C D S R V L E R Y [L] L E A K E A E
hmp11	45	S R L S Q C P E V H P [P] T P V L L [P] A V D F S L G E [W K] T Q M E E T K [A Q D I L G A V T [L] L [E] G	
hepo	51	N I T T G C A E H C S [L] N E N I T V [P] D T K V N F Y A [W K] R M E V G Q Q A V E V W Q G L A [L] L S E A	
hmp11	95	V M A A R G Q [L] G P T C L S · S [L] L G Q L S G Q [V R L [L] · [L] G A [L] Q S L [L] G T [Q] · · L P [P] Q G	
hepo	101	V L R G Q A [L] V N S S Q P W E P [L] Q L H V D K A [V] S G [L] R S [L] T T [L] L R A [L] G A [Q] K E A I S P P D	
hmp11	138	R T T A H K D P N A I F L S [F] Q H [L] R G K V R [F] L · · M L V G G S T L [C] V R R A P P T T A V P S	
hepo	151	A A S A A P L R T T A D T [F] R K [L] F R V Y S N [F] L R G K L K L Y T G E A C R T G D R	
hmp11	185	R T S L V L T N E L P N R T S G L L E T N F T A S A R T T G S G L L K W Q Q G F R A K I P G L L N	
hmp11	235	Q T S R S L D Q I P G Y L N R I H E L L N G T R G L F P G P S R R T L G A P D I S S G T S D T G S L	
hmp11	285	P P N L Q P G Y S P S P T H P P T L P P T L P V V L H P L L P D P S A P T P T P	
hmp11	335	T S P L L N T S Y T H S Q N L S Q E G	

Figure 9

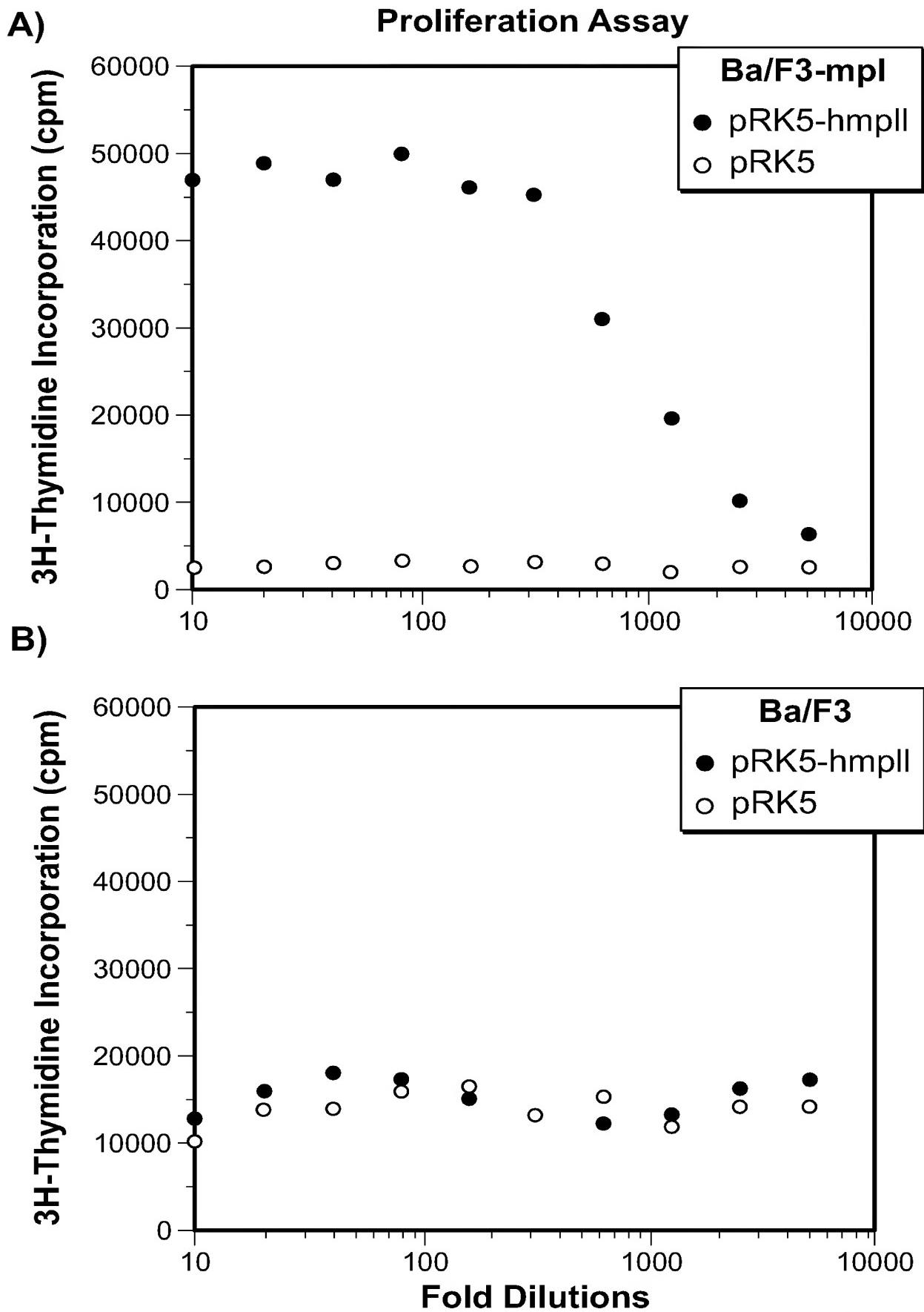


Figure 10